

FILE 'BIOSIS, MEDLINE, CAPLUS, EMBASE' ENTERED AT 10:33:25 ON 29 AUG 2002

L12 1 THYROID HORMONE RECEPTOR INTERACTOR 6  
L13 9045 THYROID HORMONE RECEPTOR  
L14 2 INTERACTOR 6  
L15 1 L13 AND L14  
L16 74124 ANTISENSE  
L17 14631 RIBOZYME  
L18 33 TRIP6  
L19 14 OIP-1  
L20 7 OPA-INTERACTING PROTEIN  
L21 23 ZYXIN-RELATED PROTEIN  
L22 13 ZRP-1  
L23 1 L18 AND L16  
L24 0 L19 AND L16  
L25 0 L18 AND L17  
L26 0 L19 AND L17  
L27 1 L20 AND L16  
L28 1 L20 AND L17  
L29 0 L21 AND L16  
L30 0 L21 AND L17  
L31 0 L22 AND L16  
L32 0 L22 AND L17

ACCESSION NUMBER: 2001:836552 CAPLUS  
DOCUMENT NUMBER: 136:81605  
TITLE: Identification of novel cofactors involved in AP-1 repression by the glucocorticoid receptor  
AUTHOR(S): Schneider, S.  
CORPORATE SOURCE: Inst. Toxikologie und Genetik, Germany  
SOURCE: Wissenschaftliche Berichte - Forschungszentrum Karlsruhe (2001), FZKA 6587, 1-139  
CODEN: WBFKF5; ISSN: 0947-8620

DOCUMENT TYPE: Report

LANGUAGE: German

AB Glucocorticoids are widely used as anti-inflammatory and immunosuppressive drugs. Within the cell they bind to the glucocorticoid receptor (GR), a ligand-dependent transcription factor (TF), which is able to modulate gene expression in various ways. Firstly, GR is able to bind directly to DNA sequences in the promotor region of hormone-inducible target genes. Secondly, GR is also able to inhibit transcriptional activity of other TFs like AP-1 and NF- $\kappa$ B. The repression of immunoregulatory genes by GR presumably is the mol. basis of the immunosuppressive effects of cortisone. The neg. crosstalk presumably involves protein-protein-interactions of GR and the other TFs. Up till now there is strong evidence that a direct binding of GR and AP-1 is not sufficient, but that addnl. factors are involved in the neg. crosstalk. The aim of this work was to identify the addnl. factors for AP-1 repression. To isolate these factors, a Two-Hybrid Screen was used to isolate GR interacting proteins. For this purpose, a GR mutant was generated which was transcriptionally inactive but still showed normal repression capacity. With the help of the Two-Hybrid Screen several previously unknown partner proteins which interact with GR in a hormone-dependent manner were identified. One of these called **Trip6** was formerly identified as a partner protein of the thyroid hormone receptor (TR) and the retinoic acid receptor (RXR), both of which are also able to repress AP-1 activity. In this work **Trip6** was functionally characterized. **Trip6** is a mainly nuclear protein, which exists in several different splice forms. The C-terminus of **Trip6** contains 3 Lim-domains, which can serve as interaction surfaces for other proteins. Besides the interaction with GR, **Trip6** also interacts with the AP-1 component cFos and the NF- $\kappa$ B subunit RelA. Moreover, **Trip6** is a transcriptional repressor, which shows no homol. to other known corepressors. Redn. of the endogenous **Trip6** protein amt. by antisense techniques showed that **Trip6** plays a key role in AP-1 repression. In conclusion the following model was developed: a multiprotein complex forms between AP-1, GR and **Trip6**. **Trip6** is thereby able to bring its repressive function into the direct environment of AP-1 and thereby inhibits transcriptional activity. As **Trip6** is also able to interact with RelA, **Trip6** may be a general factor mediating transcriptional repression by GR. This work does not only contribute to a more detailed mechanistic understanding of GR dependent AP-1 repression, but also defines a novel class of cofactors of GR.

REFERENCE COUNT: 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L27 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2002:172080 CAPLUS

DOCUMENT NUMBER: 136:211958

TITLE: Nucleic acid and corresponding protein named 85P1B3

useful in the treatment and detection of cancer

INVENTOR(S): Raitano, Arthur B.; Faris, Mary; Hubert, Rene S.;

Afar, Daniel; Ge, Wangmao; Challita-Eid, Pia;

Jakobovits, Aya

PATENT ASSIGNEE(S): Agensys, Inc., USA

SOURCE: PCT Int. Appl., 201 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

| PATENT NO.             | KIND   | DATE     | APPLICATION NO.   | DATE     |
|------------------------|--|----------|-------------------|----------|
| WO 2002018578          | A2   | 20020307 | WO 2001-US26838   | 20010828 |
| W:                     | AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM |          |                   |          |
| RW:                    | GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG   |          |                   |          |
| AU 2001088466          | A5   | 20020313 | AU 2001-88466     | 20010828 |
| PRIORITY APPLN. INFO.: |  |          | US 2000-228432P P | 20000828 |
|                        |  |          | WO 2001-US26838 W | 20010828 |

AB A novel gene (designated 85P1B3) and is encoded protein are described. To isolates genes that are involved in the progression of androgen-dependent prostate cancer to androgen-independent cancer, the suppression subtractive hybridization (SSH) procedure was used with cDNA derived from LAPC-4 androgen-dependent xenograft in male SCID mice (3 days post-castration vs. no castration). The 85P1B3 SSH cDNA sequence is a fragment of the **Opa-interacting protein 5** gene (OIP-5). A 85P1B3 cDNA clone of 1262 bp was isolated by screening a human testis library, revealing an ORF of 229 amino acids. The 85P1B3 nucleotide and protein sequence correspond to the OIP-5 gene, the protein is predicted to be localized to the cytoplasmic, and the gene was localized to chromosome 15q13.2-q14 (a region implicated in cancers). The restricted expression of 85P1B3 in normal tissues, and the expression detected in bladder cancer, kidney cancer, colon cancer, lung, cancer, prostate cancer, ovarian cancer, and breast cancer indicate that 85P1B3 is a therapeutic and/or prophylactic target and a prognostic and/or diagnostic marker for human cancer. The 85P1B3 gene or fragment thereof, or its encoded protein or a fragment thereof, can be used to elicit an immune response.

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=> d ibib, abs

L15 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2001:763247 CAPLUS

DOCUMENT NUMBER: 135:314406

TITLE: Cancer diagnosis via gene expression profiles

INVENTOR(S): Inoue, Hiroshi; Matsuyama, Ayumi; Mimori, Koshi; Mori, Masaki; Mineno, Junichi; Yoshikawa, Yoshie; Mukai, Hiroyuki; Asada, Kiyozo; Kato, Ikunoshin

PATENT ASSIGNEE(S): Takara Shuzo Co., Ltd., Japan

SOURCE: PCT Int. Appl., 105 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: Japanese

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

| PATENT NO.    | KIND   | DATE     | APPLICATION NO. | DATE     |
|---------------|--|----------|-----------------|----------|
| WO 2001077385 | A1   | 20011018 | WO 2001-JP3031  | 20010409 |
| W:            | AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM |          |                 |          |
| RW:           | GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG   |          |                 |          |

PRIORITY APPLN. INFO.: JP 2000-109982 A 20000411

JP 2000-306434 A 20001005

AB A method of evaluating the malignancy of cancer (in particular, gastric cancer) or cancer diagnosis (in particular, gastric cancer) based on the expression levels of at least 8 genes, each showing a change in expression level depending on the malignancy of gastric cancer, or difference in expression between a test sample and a control sample; is disclosed. The method includes hybridization and nucleic acid amplification such as PCR, RT-PCR, , and use antibodies in immunoassays to quantify the gene product. Cluster anal. of gene expression patterns, including comparison with expression of housekeeping genes, is used. A kit and DNA microarrays having the above genes immobilized on a support, are claimed.

REFERENCE COUNT: 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

**WEST****Freeform Search****Database:**

US Patents Full-Text Database  
US Pre-Grant Publication Full-Text Database  
JPO Abstracts Database  
EPO Abstracts Database  
Derwent World Patents Index  
IBM Technical Disclosure Bulletins

**Term:**

interactor 6

**Display:**  **Documents in Display Format:**  **Starting with Number** **Generate:** ☐ Hit List ☒ Hit Count ☐ Side by Side ☐ Image

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**Search History**

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**DATE:** Thursday, August 29, 2002   [Printable Copy](#)   [Create Case](#)

| <u>Set Name</u><br>side by side                      | <u>Query</u>                        | <u>Hit Count</u> | <u>Set Name</u><br>result set |
|--|-------------------------------------|------------------|-------------------------------|
| <i>DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=ADJ</i> |                                     |                  |                               |
| <u>L13</u>   | L12 and 6                           | 182              | <u>L13</u>                    |
| <u>L12</u>   | L1 and L8                           | 182              | <u>L12</u>                    |
| <u>L11</u>   | thyroid hormone receptor interactor | 0                | <u>L11</u>                    |
| <u>L10</u>   | L1 and L2                           | 1                | <u>L10</u>                    |
| <u>L9</u>  | ribozyme                            | 7535             | <u>L9</u>                     |
| <u>L8</u>  | antisense                           | 23182            | <u>L8</u>                     |
| <u>L7</u>  | zrp-1                               | 1                | <u>L7</u>                     |
| <u>L6</u>  | zyxin-related protein               | 1                | <u>L6</u>                     |
| <u>L5</u>  | OIP-1                               | 1                | <u>L5</u>                     |
| <u>L4</u>  | opa-interacting protein             | 0                | <u>L4</u>                     |
| <u>L3</u>  | TRIP6                               | 3                | <u>L3</u>                     |
| <u>L2</u>  | interactor 6                        | 2                | <u>L2</u>                     |
| <u>L1</u>  | thyroid hormone receptor            | 532              | <u>L1</u>                     |

END OF SEARCH HISTORY

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(FILE 'HOME' ENTERED AT 10:20:08 ON 29 AUG 2002)

FILE 'REGISTRY' ENTERED AT 10:20:17 ON 29 AUG 2002

FILE 'CAPLUS' ENTERED AT 10:20:20 ON 29 AUG 2002  
S CTCCAGACAGCGGTCTTGAA/SQSN

L1 FILE 'REGISTRY' ENTERED AT 10:21:44 ON 29 AUG 2002  
1 S GTCCAGACAGCGGTCTTGAA/SQSN

SEQ ID #13

L2 FILE 'CAPLUS' ENTERED AT 10:24:31 ON 29 AUG 2002  
1 S L1  
S GCCCAGAAGCCTGAGAGGCT/SQSN

L3 FILE 'REGISTRY' ENTERED AT 10:25:48 ON 29 AUG 2002  
0 S GCCCAGAAGCCTGAGAGGCT/SQSN

SEQ ID #25

L4 FILE 'CAPLUS' ENTERED AT 10:27:10 ON 29 AUG 2002  
0 S L3  
S TATGGCCCCACCGCACACTG/SQSN

L5 FILE 'REGISTRY' ENTERED AT 10:27:40 ON 29 AUG 2002  
79 S TATGGCCCCACCGCACACTG/SQSN

SEQ ID #49

L6 FILE 'CAPLUS' ENTERED AT 10:28:16 ON 29 AUG 2002  
12 S L5  
L7 2 DUP REM L6 (10 DUPLICATES REMOVED)  
S AGGAAGACTCAGCAGTCAGT/SQSN

L8 FILE 'REGISTRY' ENTERED AT 10:30:17 ON 29 AUG 2002  
112 S AGGAAGACTCAGCAGTCAGT/SQSN

SEQ ID #69

L9 FILE 'CAPLUS' ENTERED AT 10:30:46 ON 29 AUG 2002  
13 S L8  
S GTAACAATGACTGGGCCTGT/SQSN

L10 FILE 'REGISTRY' ENTERED AT 10:31:37 ON 29 AUG 2002  
1 S GTAACAATGACTGGGCCTGT/SQSN

SEQ ID #88

L11 FILE 'CAPLUS' ENTERED AT 10:31:57 ON 29 AUG 2002  
1 S L10

hit:

SEQ ID NO: 13 & 88

L2 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2001:250041 CAPLUS

DOCUMENT NUMBER: 135:327983

TITLE: Comparative analysis of the gene-dense ACHE/TFR2 region on human chromosome 7q22 with the orthologous region on mouse chromosome 5

AUTHOR(S): Wilson, Michael D.; Riemer, Cathy; Martindale, Duane W.; Schnupf, Pamela; Boright, Andrew P.; Cheung, Tony L.; Hardy, Daniel M.; Schwartz, Scott; Scherer, Stephen W.; Tsui, Lap-Chee; Miller, Webb; Koop, Ben F.

CORPORATE SOURCE: Department of Biology, University of Victoria, Victoria, BC, V8W 3N5, Can.

SOURCE: Nucleic Acids Research (2001), 29(6), 1352-1365

CODEN: NARHAD; ISSN: 0305-1048

PUBLISHER: Oxford University Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Chromosome 7q22 has been the focus of many cytogenetic and mol. studies aimed at delineating regions commonly deleted in myeloid leukemias and myelodysplastic syndromes. We have compared a gene-dense, GC-rich sub-region of 7q22 with the orthologous region on mouse chromosome 5. A phys. map of 640 kb of genomic DNA from mouse chromosome 5 was derived from a series of over-lapping bacterial artificial chromosomes. A 296 kb segment from the phys. map, spanning Ache to Tfr2, was compared with 267 kb of human sequence. We identified a conserved linkage of 12 genes including an open reading frame flanked by Ache and Asr2, a novel cation-chloride cotransporter interacting protein Cipl, Ephb4, Zan and Perq1. While some of these genes have been previously described, in each case we present new data derived from our comparative sequence anal. Adjacent unfinished sequence data from the mouse contains an orthologous block of 10 addnl. genes including three novel cDNA sequences that we subsequently mapped to human 7q22. Methods for displaying comparative genomic information, including unfinished sequence data, are becoming increasingly important. We supplement our printed comparative anal. with a new, Web-based program called Laj (local alignments with java). Laj provides interactive access to archived pairwise sequence alignments via the WWW. It displays synchronized views of a dot-plot, a percent identity plot, a nucleotide-level local alignment and a variety of relevant annotations. Our mouse-human comparison can be viewed at <http://web.uvic.ca/-bioweb/laj.html>. Laj is available at <http://bio.cse.psu.edu/>, along with online documentation and addnl. examples of annotated genomic regions.

REFERENCE COUNT: 76 THERE ARE 76 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT



=> d ibib, abs L6, all

L6 ANSWER 1 OF 12 CAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2002:372178 CAPLUS

DOCUMENT NUMBER: 136:381072

TITLE: The contribution of 700,000 ORF sequence tags to the definition of the human transcriptome

AUTHOR(S): Camargo, Anamaria A.; Samaia, Helena P. B.; Dias-Neto, Emmanuel; Simao, Daniel F.; Migotto, Italo A.; Briones, Marcelo R. S.; Costa, Fernando F.; Nagai, Maria Aparecida; Verjovski-Almeida, Sergio; Zago, Marco A.; Andrade, Luis Eduardo C.; Carrer, Helaine; El-Dorry, Hamza F. A.; Espreafico, Enilza M.; Habr-Gama, Angelita; Giannella-Neto, Daniel; Goldman, Gustavo H.; Gruber, Arthur; Hackel, Christine; Kimura, Edna T.; Maciel, Rui M. B.; Marie, Suely K. N.; Martins, Elizabeth A. L.; Nobrega, Marina P.; Paco-Larson, Maria Luisa; Pardini, Maria Ines M. C.; Pereira, Goncalo G.; Pesquero, Joao Bosco; Rodrigues, Vanderlei; Rogatto, Silvia R.; Da Silva, Ismael D. C. G.; Sogayar, Mari C.; Sonati, Maria De Fatima; Tajara, Eloiza H.; Valentini, Sandro R.; Alberto, Fernando L.; Amaral, Maria Elisabete J.; Aneas, Ivy; Arnaldi, Lilliane A. T.; De Assis, Angela M.; Bengtson, Mario Henrique; Bergamo, Nadia Aparecida; Bombonato, Vanessa; De Camargo, Maria E. R.; Canevari, Renata A.; Carraro, Dirce M.; Cerutti, Janete M.; Correa, Maria Lucia C.; Correa, Rosana F. R.; Costa, Maria Cristina R.; Curcio, Cyntia; Hokama, Paula O. M.; Ferreira, Ari J. S.; Furuzawa, Gilberto K.; Gushiken, Tsieko; Ho, Paulo L.; Kimura, Elza; Krieger, Jose E.; Leite, Luciana C. C.; Majumder, Paromita; Marins, Mozart; Marques, Everaldo R.; Melo, Analy S. A.; Melo, Monica; Mestriner, Carlos Alberto; Miracca, Elisabete C.; Miranda, Daniela C.; Nascimento, Ana Lucia T. O.; Nobrega, Francisco G.; Ojopi, Elida P. B.; Pandolfi, Jose Rodrigo C.; Pessoa, Luciana G.; Prevedel, Aline C.; Rahal, Paula; Rainho, Claudia A.; Reis, Eduardo M. R.; Ribeiro, Marcelo L.; Da Ros, Nancy; De Sa, Renata G.; Sales, Magaly M.; Sant'anna, Simone Cristina; Dos Santos, Mariana L.; Da Silva, Aline M.; Da Silva, Neusa P.; Silva, Wilson A., Jr.; Da Silveira, Rosana A.; Sousa, Josane F.; Stecconi, Daniella; Tsukumo, Fernando; Valente, Valeria; Soares, Fernando; Moreira, Eloisa S.; Nunes, Diana N.; Correa, Ricardo G.; Zalcborg, Heloisa; Carvalho, Alex F.; Reis, Luis F. L.; Brentani, Ricardo R.; Simpson, Andrew J. G.; De Souza, Sandro J.

CORPORATE SOURCE: Ludwig Institute for Cancer Research, Sao Paulo, 01509-010, Brazil

SOURCE: Proceedings of the National Academy of Sciences of the United States of America (2001), 98(21), 12103-12108  
CODEN: PNASA6; ISSN: 0027-8424

PUBLISHER: National Academy of Sciences

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Open reading frame expressed sequences tags (ORESTES) differ from conventional ESTs by providing sequence data from the central protein coding portion of transcripts. A total of 696,745 ORESTES sequences were generated from 24 human tissues and a subset of the data that correspond to a set of 15,095 full-length mRNAs used as a means of assessing the efficiency of the strategy and its potential contribution to the definition of the human transcriptome. It was estd. that ORESTES sampled over 80% of all highly and moderately expressed, and between 40% and 50%

of rarely expressed, human genes. In the most thoroughly sequenced tissue, the breast, the 130,000 ORESTES generated are derived from transcripts from an estd. 70% of all genes expressed in that tissue, with an equally efficient representation of both highly and poorly expressed genes. In this respect, the capacity of the ORESTES strategy both for gene discovery and shotgun transcript sequence generation significantly exceeds that of conventional ESTs. The distribution of ORESTES is such that many human transcripts are now represented by a scaffold of partial sequences distributed along the length of each gene product. The exptl. joining of the scaffold components, by reverse transcription-PCR, represents a direct route to transcript finishing that may represent a useful alternative to full-length cDNA cloning. [This abstr. record is one of many records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

AN 2002:372178 CAPLUS

DN 136:381072

TI The contribution of 700,000 ORF sequence tags to the definition of the human transcriptome

AU Camargo, Anamaria A.; Samaia, Helena P. B.; Dias-Neto, Emmanuel; Simao, Daniel F.; Migotto, Italo A.; Briones, Marcelo R. S.; Costa, Fernando F.; Nagai, Maria Aparecida; Verjovski-Almeida, Sergio; Zago, Marco A.; Andrade, Luis Eduardo C.; Carrer, Helaine; El-Dorry, Hamza F. A.; Espreafico, Enilza M.; Habr-Gama, Angelita; Giannella-Neto, Daniel; Goldman, Gustavo H.; Gruber, Arthur; Hackel, Christine; Kimura, Edna T.; Maciel, Rui M. B.; Marie, Suely K. N.; Martins, Elizabeth A. L.; Nobrega, Marina P.; Paco-Larson, Maria Luisa; Pardini, Maria Ines M. C.; Pereira, Goncalo G.; Pesquero, Joao Bosco; Rodrigues, Vanderlei; Rogatto, Silvia R.; Da Silva, Ismael D. C. G.; Sogayar, Mari C.; Sonati, Maria De Fatima; Tajara, Eloiza H.; Valentini, Sandro R.; Alberto, Fernando L.; Amaral, Maria Elisabete J.; Aneas, Ivy; Arnaldi, Liliane A. T.; De Assis, Angela M.; Bengtson, Mario Henrique; Bergamo, Nadia Aparecida; Bombonato, Vanessa; De Camargo, Maria E. R.; Canevari, Renata A.; Carraro, Dirce M.; Cerutti, Janete M.; Correa, Maria Lucia C.; Correa, Rosana F. R.; Costa, Maria Cristina R.; Curcio, Cyntia; Hokama, Paula O. M.; Ferreira, Ari J. S.; Furuzawa, Gilberto K.; Gushiken, Tsieko; Ho, Paulo L.; Kimura, Elza; Krieger, Jose E.; Leite, Luciana C. C.; Majumder, Paromita; Marins, Mozart; Marques, Everaldo R.; Melo, Analy S. A.; Melo, Monica; Mestriner, Carlos Alberto; Miracca, Elisabete C.; Miranda, Daniela C.; Nascimento, Ana Lucia T. O.; Nobrega, Francisco G.; Ojopi, Elida P. B.; Pandolfi, Jose Rodrigo C.; Pessoa, Luciana G.; Prevedel, Aline C.; Rahal, Paula; Rainho, Claudia A.; Reis, Eduardo M. R.; Ribeiro, Marcelo L.; Da Ros, Nancy; De Sa, Renata G.; Sales, Magaly M.; Sant'anna, Simone Cristina; Dos Santos, Mariana L.; Da Silva, Aline M.; Da Silva, Neusa P.; Silva, Wilson A., Jr.; Da Silveira, Rosana A.; Sousa, Josane F.; Stecconi, Daniella; Tsukumo, Fernando; Valente, Valeria; Soares, Fernando; Moreira, Eloisa S.; Nunes, Diana N.; Correa, Ricardo G.; Zalcborg, Heloisa; Carvalho, Alex F.; Reis, Luis F. L.; Brentani, Ricardo R.; Simpson, Andrew J. G.; De Souza, Sandro J.

CS Ludwig Institute for Cancer Research, Sao Paulo, 01509-010, Brazil

SO Proceedings of the National Academy of Sciences of the United States of America (2001), 98(21), 12103-12108  
CODEN: PNASA6; ISSN: 0027-8424

PB National Academy of Sciences

DT Journal

LA English

CC 3-3 (Biochemical Genetics)

Section cross-reference(s): 13

AB Open reading frame expressed sequences tags (ORESTES) differ from conventional ESTs by providing sequence data from the central protein coding portion of transcripts. A total of 696,745 ORESTES sequences were generated from 24 human tissues and a subset of the data that correspond to a set of 15,095 full-length mRNAs used as a means of assessing the efficiency of the strategy and its potential contribution to the

definition of the human transcriptome. It was estd. that ORESTES sampled over 80% of all highly and moderately expressed, and between 40% and 50% of rarely expressed, human genes. In the most thoroughly sequenced tissue, the breast, the 130,000 ORESTES generated are derived from transcripts from an estd. 70% of all genes expressed in that tissue, with an equally efficient representation of both highly and poorly expressed genes. In this respect, the capacity of the ORESTES strategy both for gene discovery and shotgun transcript sequence generation significantly exceeds that of conventional ESTs. The distribution of ORESTES is such that many human transcripts are now represented by a scaffold of partial sequences distributed along the length of each gene product. The exptl. joining of the scaffold components, by reverse transcription-PCR, represents a direct route to transcript finishing that may represent a useful alternative to full-length cDNA cloning. [This abstr. record is one of many records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

- ST transcriptome human ORF sequence tag; gene expression discovery ORF sequence tag human; EST sequence gene discovery human transcriptome; expressed sequence tag human transcriptome
- IT Genetic element  
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)  
 (ORESTES (open reading frame expressed sequence tags); contribution of 700,000 ORF sequence tags to the definition of the human transcriptome)
- IT Bioinformatics  
 Human  
 cDNA sequences  
 (contribution of 700,000 ORF sequence tags to the definition of the human transcriptome)
- IT Gene, animal  
 RL: BSU (Biological study, unclassified); BIOL (Biological study)  
 (contribution of 700,000 ORF sequence tags to the definition of the human transcriptome)
- IT EST (expressed sequence tag)  
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)  
 (contribution of 700,000 ORF sequence tags to the definition of the human transcriptome)
- IT Genetic methods  
 (gene discovery; contribution of 700,000 ORF sequence tags to the definition of the human transcriptome)
- IT 316335-64-5, GenBank BF886901 316335-65-6, GenBank BF886902  
 316335-66-7, GenBank BF886903 316335-67-8, GenBank BF886904  
 316335-68-9, GenBank BF886905 316335-69-0, GenBank BF886906  
 316335-70-3, GenBank BF886907 316335-71-4, GenBank BF886908  
 316335-72-5, GenBank BF886909 316335-73-6, GenBank BF886910  
 316335-74-7, GenBank BF886911 316335-75-8, GenBank BF886912  
 316335-76-9, GenBank BF886913 316335-77-0, GenBank BF886914  
 316335-78-1, GenBank BF886915 316335-79-2, GenBank BF886916  
 316335-80-5, GenBank BF886917 316335-81-6, GenBank BF886918  
 316335-82-7, GenBank BF886919 316335-83-8, GenBank BF886920  
 316335-84-9, GenBank BF886921 316335-85-0, GenBank BF886922  
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| 316337-96-9, GenBank BF887133 | 316337-97-0, GenBank BF887134 |
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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(nucleotide sequence; contribution of 700,000 ORF sequence tags to the definition of the human transcriptome)

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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(nucleotide sequence; contribution of 700,000 ORF sequence tags to the definition of the human transcriptome)

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| 316400-69-8, GenBank BF887423    | 316400-70-1, GenBank BF887424 |
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| 316401-33-9, | GenBank | BF887487 | 316401-34-0, | GenBank | BF887488 |
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| 316401-81-7, | GenBank | BF887536 | 316401-82-8, | GenBank | BF887537 |
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| 316402-25-2, GenBank BF887580 | 316402-26-3, GenBank BF887581 |
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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(nucleotide sequence; contribution of 700,000 ORF sequence tags to the definition of the human transcriptome)

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| 316403-98-2, GenBank BF887755 | 316403-99-3, GenBank BF887756 |
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| 316404-60-1, GenBank BF887817 | 316404-61-2, GenBank BF887818 |
| 316404-62-3, GenBank BF887819 | 316404-63-4, GenBank BF887820 |
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| 316404-67-8, | GenBank | BF887824 | 316404-68-9, | GenBank | BF887825 |
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| 316404-71-4, | GenBank | BF887828 | 316404-72-5, | GenBank | BF887829 |
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| 316404-77-0, | GenBank | BF887834 | 316404-78-1, | GenBank | BF887835 |
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| 316404-81-6, | GenBank | BF887838 | 316404-82-7, | GenBank | BF887839 |
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| 316404-87-2, | GenBank | BF887844 | 316404-88-3, | GenBank | BF887845 |
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| 316404-97-4, | GenBank | BF887854 | 316404-98-5, | GenBank | BF887855 |

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(nucleotide sequence; contribution of 700,000 ORF sequence tags to the definition of the human transcriptome)

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| 316405-07-9,    | GenBank | BF887864 | 316405-08-0, | GenBank | BF887865 |
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| 316407-35-9, GenBank BF888092 | 316407-36-0, GenBank BF888093 |

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(nucleotide sequence; contribution of 700,000 ORF sequence tags to the definition of the human transcriptome)

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| 316408-93-2, | GenBank | BF888265 | 316408-94-3, | GenBank | BF888266 |
| 316408-95-4, | GenBank | BF888267 | 316408-96-5, | GenBank | BF888268 |
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| 316409-73-1, GenBank BF888229 | 316409-74-2, GenBank BF888230 |

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(nucleotide sequence; contribution of 700,000 ORF sequence tags to the definition of the human transcriptome)

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| 316410-67-0, GenBank BF888428        | 316410-68-1, GenBank BF888429 |
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| 316410-77-2, GenBank BF888438        | 316410-78-3, GenBank BF888439 |
| 316410-79-4, GenBank BF888440        | 316410-80-7, GenBank BF888441 |
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| 316411-03-7, | GenBank | BF888464 | 316411-04-8, | GenBank | BF888465 |
| 316411-05-9, | GenBank | BF888466 | 316411-06-0, | GenBank | BF888467 |
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| 316411-19-5, | GenBank | BF888480 | 316411-20-8, | GenBank | BF888481 |
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| 316411-65-1, | GenBank | BF888526 | 316411-66-2, | GenBank | BF888527 |
| 316411-67-3, | GenBank | BF888528 | 316411-68-4, | GenBank | BF888529 |
| 316411-69-5, | GenBank | BF888530 | 316411-70-8, | GenBank | BF888531 |
| 316411-71-9, | GenBank | BF888532 | 316411-72-0, | GenBank | BF888533 |
| 316411-73-1, | GenBank | BF888534 | 316411-74-2, | GenBank | BF888535 |
| 316411-75-3, | GenBank | BF888536 | 316411-76-4, | GenBank | BF888537 |
| 316411-77-5, | GenBank | BF888538 | 316411-78-6, | GenBank | BF888539 |
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| 316411-89-9, | GenBank | BF888641 | 316411-90-2, | GenBank | BF888642 |
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| 316411-97-9, | GenBank | BF888649 | 316411-98-0, | GenBank | BF888650 |
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| 316412-01-8, | GenBank | BF888653 | 316412-02-9, | GenBank | BF888654 |
| 316412-03-0, | GenBank | BF888655 | 316412-04-1, | GenBank | BF888656 |
| 316412-05-2, | GenBank | BF888657 | 316412-06-3, | GenBank | BF888658 |
| 316412-07-4, | GenBank | BF888659 | 316412-08-5, | GenBank | BF888660 |
| 316412-09-6, | GenBank | BF888661 | 316412-10-9, | GenBank | BF888662 |



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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL  
(Biological study)

(nucleotide sequence; contribution of 700,000 ORF sequence tags to the  
definition of the human transcriptome)

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|    | 316413-05-5, GenBank BF888562 | 316413-06-6, GenBank BF888563 |
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|    | 316413-11-3, GenBank BF888568 | 316413-12-4, GenBank BF888569 |
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| 316413-37-3, | GenBank | BF888594 | 316413-38-4, | GenBank | BF888595 |
| 316413-39-5, | GenBank | BF888596 | 316413-40-8, | GenBank | BF888597 |
| 316413-41-9, | GenBank | BF888598 | 316413-42-0, | GenBank | BF888599 |
| 316413-43-1, | GenBank | BF888600 | 316413-44-2, | GenBank | BF888601 |
| 316413-45-3, | GenBank | BF888602 | 316413-46-4, | GenBank | BF888603 |
| 316413-47-5, | GenBank | BF888604 | 316413-48-6, | GenBank | BF888605 |
| 316413-49-7, | GenBank | BF888606 | 316413-50-0, | GenBank | BF888607 |
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| 316413-53-3, | GenBank | BF888610 | 316413-54-4, | GenBank | BF888611 |
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| 316413-57-7, | GenBank | BF888614 | 316413-58-8, | GenBank | BF888615 |
| 316413-59-9, | GenBank | BF888616 | 316413-60-2, | GenBank | BF888617 |
| 316413-61-3, | GenBank | BF888618 | 316413-62-4, | GenBank | BF888619 |
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| 316413-65-7, | GenBank | BF888622 | 316413-66-8, | GenBank | BF888623 |
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| 316413-79-3, | GenBank | BF888740 | 316413-80-6, | GenBank | BF888741 |
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| 316413-89-5, | GenBank | BF888750 | 316413-90-8, | GenBank | BF888751 |
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| 316413-95-3, | GenBank | BF888756 | 316413-96-4, | GenBank | BF888757 |
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| 316413-99-7, | GenBank | BF888760 | 316414-00-3, | GenBank | BF888761 |
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| 316414-17-2, | GenBank | BF888778 | 316414-18-3, | GenBank | BF888779 |
| 316414-19-4, | GenBank | BF888780 | 316414-20-7, | GenBank | BF888781 |
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| 316414-41-2, | GenBank | BF888802 | 316414-42-3, | GenBank | BF888803 |
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| 316414-45-6, | GenBank | BF888806 | 316414-46-7, | GenBank | BF888807 |
| 316414-47-8, | GenBank | BF888808 | 316414-48-9, | GenBank | BF888809 |
| 316414-49-0, | GenBank | BF888810 | 316414-50-3, | GenBank | BF888811 |

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(nucleotide sequence; contribution of 700,000 ORF sequence tags to the definition of the human transcriptome)

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|    | 316414-55-8, | GenBank | BF888816 | 316414-56-9, | GenBank | BF888817 |
|    | 316414-57-0, | GenBank | BF888818 | 316414-58-1, | GenBank | BF888819 |
|    | 316414-59-2, | GenBank | BF888820 | 316414-60-5, | GenBank | BF888821 |
|    | 316414-61-6, | GenBank | BF888822 | 316414-62-7, | GenBank | BF888823 |
|    | 316414-63-8, | GenBank | BF888824 | 316414-64-9, | GenBank | BF888825 |
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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(nucleotide sequence; contribution of 700,000 ORF sequence tags to the definition of the human transcriptome)

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| 316419-09-7, | GenBank | BF889271 | 316419-10-0, | GenBank | BF889272 |
| 316419-11-1, | GenBank | BF889273 | 316419-12-2, | GenBank | BF889274 |
| 316419-13-3, | GenBank | BF889275 | 316419-14-4, | GenBank | BF889276 |
| 316419-15-5, | GenBank | BF889277 | 316419-16-6, | GenBank | BF889278 |
| 316419-17-7, | GenBank | BF889279 | 316419-18-8, | GenBank | BF889280 |
| 316419-19-9, | GenBank | BF889281 | 316419-20-2, | GenBank | BF889282 |
| 316419-21-3, | GenBank | BF889283 | 316419-22-4, | GenBank | BF889284 |
| 316419-23-5, | GenBank | BF889285 | 316419-24-6, | GenBank | BF889286 |
| 316419-25-7, | GenBank | BF889287 | 316419-26-8, | GenBank | BF889288 |

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(nucleotide sequence; contribution of 700,000 ORF sequence tags to the definition of the human transcriptome)

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|    | 316419-33-7, | GenBank | BF889295 | 316419-34-8, | GenBank | BF889296 |
|    | 316419-35-9, | GenBank | BF889297 | 316419-36-0, | GenBank | BF889298 |
|    | 316419-37-1, | GenBank | BF889299 | 316419-38-2, | GenBank | BF889300 |
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| 316419-55-3, | GenBank | BF889317 | 316419-56-4, | GenBank | BF889318 |
| 316419-57-5, | GenBank | BF889319 | 316419-58-6, | GenBank | BF889320 |
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| 316420-07-2, | GenBank | BF889369 | 316420-08-3, | GenBank | BF889370 |
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| 316420-21-0, | GenBank | BF889383 | 316420-22-1, | GenBank | BF889384 |
| 316420-23-2, | GenBank | BF889385 | 316420-24-3, | GenBank | BF889386 |
| 316420-25-4, | GenBank | BF889387 | 316420-26-5, | GenBank | BF889388 |
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| 316420-37-8, | GenBank | BF889399 | 316420-38-9, | GenBank | BF889400 |
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| 316420-69-6, | GenBank | BF889431 | 316430-66-7, | GenBank | BF890486 |
| 316430-67-8, | GenBank | BF890487 | 316430-68-9, | GenBank | BF890488 |
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| 316430-75-8, | GenBank | BF890495 | 316430-76-9, | GenBank | BF890496 |
| 316430-77-0, | GenBank | BF890497 | 316430-78-1, | GenBank | BF890498 |
| 316430-79-2, | GenBank | BF890499 | 316430-80-5, | GenBank | BF890500 |
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| 316430-85-0, | GenBank | BF890505 | 316430-86-1, | GenBank | BF890506 |
| 316430-87-2, | GenBank | BF890507 | 316430-88-3, | GenBank | BF890508 |
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| 316430-91-8, | GenBank | BF890511 | 316430-92-9, | GenBank | BF890512 |
| 316430-93-0, | GenBank | BF890513 | 316430-94-1, | GenBank | BF890514 |
| 316430-95-2, | GenBank | BF890515 | 316430-96-3, | GenBank | BF890516 |
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| 316431-05-7, | GenBank | BF890525 | 316431-06-8, | GenBank | BF890526 |
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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(nucleotide sequence; contribution of 700,000 ORF sequence tags to the definition of the human transcriptome)

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|    | 316431-69-3, | GenBank | BF890589 | 316431-70-6, | GenBank | BF890590 |
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|    | 316431-73-9, | GenBank | BF890593 | 316431-74-0, | GenBank | BF890594 |
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|    | 316431-77-3, | GenBank | BF890597 | 316431-78-4, | GenBank | BF890598 |
|    | 316431-79-5, | GenBank | BF890599 | 316431-80-8, | GenBank | BF890600 |
|    | 316431-81-9, | GenBank | BF890601 | 316431-82-0, | GenBank | BF890602 |
|    | 316431-83-1, | GenBank | BF890603 | 316431-84-2, | GenBank | BF890604 |
|    | 316431-85-3, | GenBank | BF890605 | 316431-86-4, | GenBank | BF890606 |
|    | 316431-87-5, | GenBank | BF890607 | 316431-88-6, | GenBank | BF890608 |
|    | 316431-89-7, | GenBank | BF890609 | 316431-90-0, | GenBank | BF890610 |



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| 316431-97-7, | GenBank | BF890617 | 316431-98-8, | GenBank | BF890618 |
| 316431-99-9, | GenBank | BF890619 | 316432-00-5, | GenBank | BF890620 |
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| 316432-13-0, | GenBank | BF890633 | 316432-14-1, | GenBank | BF890634 |
| 316432-15-2, | GenBank | BF890635 | 316432-16-3, | GenBank | BF890636 |
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| 316432-45-8, | GenBank | BF890665 | 316432-46-9, | GenBank | BF890666 |
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| 316432-61-8, | GenBank | BF890681 | 316432-62-9, | GenBank | BF890682 |
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| 316432-69-6, | GenBank | BF890689 | 316432-70-9, | GenBank | BF890690 |
| 316432-71-0, | GenBank | BF890691 | 316432-72-1, | GenBank | BF890692 |
| 316432-73-2, | GenBank | BF890693 | 316432-74-3, | GenBank | BF890694 |
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| 316432-77-6, | GenBank | BF890697 | 316432-78-7, | GenBank | BF890698 |
| 316432-79-8, | GenBank | BF890699 | 316432-80-1, | GenBank | BF890701 |
| 316432-81-2, | GenBank | BF890702 | 316432-82-3, | GenBank | BF890703 |
| 316432-83-4, | GenBank | BF890704 | 316432-84-5, | GenBank | BF890705 |
| 316432-85-6, | GenBank | BF890706 | 316432-86-7, | GenBank | BF890707 |
| 316432-87-8, | GenBank | BF890708 | 316432-88-9, | GenBank | BF890709 |
| 316432-89-0, | GenBank | BF890710 | 316432-90-3, | GenBank | BF890711 |
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| 316432-95-8, | GenBank | BF890716 | 316432-96-9, | GenBank | BF890717 |
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| 316433-07-5, | GenBank | BF890728 | 316433-08-6, | GenBank | BF890729 |
| 316433-09-7, | GenBank | BF890730 | 316433-10-0, | GenBank | BF890735 |
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| 316433-13-3, | GenBank | BF890738 | 316433-14-4, | GenBank | BF890739 |
| 316433-15-5, | GenBank | BF890740 | 316433-16-6, | GenBank | BF890741 |
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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(nucleotide sequence; contribution of 700,000 ORF sequence tags to the definition of the human transcriptome)

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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(nucleotide sequence; contribution of 700,000 ORF sequence tags to the definition of the human transcriptome)

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| 316437-79-3, | GenBank | BF891206 | 316437-80-6, | GenBank | BF891207 |
| 316437-81-7, | GenBank | BF891208 | 316437-82-8, | GenBank | BF891209 |
| 316437-83-9, | GenBank | BF891210 | 316437-84-0, | GenBank | BF891211 |
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| 316438-63-8, GenBank BF891290 | 316438-64-9, GenBank BF891291 |
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| 316438-71-8, GenBank BF891298 | 316438-72-9, GenBank BF891299 |
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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(nucleotide sequence; contribution of 700,000 ORF sequence tags to the definition of the human transcriptome)

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| 316438-77-4, GenBank BF891304    | 316438-78-5, GenBank BF891305 |
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| 316438-87-6, GenBank BF891314    | 316438-88-7, GenBank BF891315 |
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| 316439-45-9, | GenBank | BF891372 | 316439-46-0, | GenBank | BF891373 |
| 316439-47-1, | GenBank | BF891374 | 316439-48-2, | GenBank | BF891375 |
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| 316439-63-1, | GenBank | BF891390 | 316439-64-2, | GenBank | BF891391 |
| 316439-65-3, | GenBank | BF891392 | 316439-66-4, | GenBank | BF891393 |
| 316439-67-5, | GenBank | BF891394 | 316439-68-6, | GenBank | BF891395 |
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| 316439-95-9, | GenBank | BF891423 | 316439-96-0, | GenBank | BF891424 |
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| 316440-09-2, | GenBank | BF891437 | 316440-10-5, | GenBank | BF891438 |
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| 316440-17-2, | GenBank | BF891445 | 316440-18-3, | GenBank | BF891446 |
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| 316440-47-8, | GenBank | BF891475 | 316440-48-9, | GenBank | BF891476 |
| 316440-49-0, | GenBank | BF891477 | 316440-50-3, | GenBank | BF891478 |
| 316440-51-4, | GenBank | BF891479 | 316440-52-5, | GenBank | BF891480 |
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| 316440-55-8, | GenBank | BF891483 | 316440-56-9, | GenBank | BF891484 |
| 316440-57-0, | GenBank | BF891485 | 316440-58-1, | GenBank | BF891486 |
| 316440-59-2, | GenBank | BF891487 | 316440-60-5, | GenBank | BF891488 |
| 316440-61-6, | GenBank | BF891489 | 316440-62-7, | GenBank | BF891490 |

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| 316440-71-8, | GenBank | BF891512 | 316440-72-9, | GenBank | BF891513 |
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| 316440-75-2, | GenBank | BF891516 | 316440-76-3, | GenBank | BF891517 |
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| 316441-01-7, | GenBank | BF891529 | 316441-02-8, | GenBank | BF891530 |
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| 316441-11-9, | GenBank | BF891539 | 316441-12-0, | GenBank | BF891540 |

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(nucleotide sequence; contribution of 700,000 ORF sequence tags to the definition of the human transcriptome)

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|    | 316441-17-5, | GenBank | BF891545 | 316441-18-6, | GenBank | BF891546 |
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|    | 316441-21-1, | GenBank | BF891549 | 316441-22-2, | GenBank | BF891550 |
|    | 316441-23-3, | GenBank | BF891551 | 316441-24-4, | GenBank | BF891552 |
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|    | 316441-35-7, | GenBank | BF891563 | 316441-36-8, | GenBank | BF891564 |
|    | 316441-37-9, | GenBank | BF891565 | 316441-38-0, | GenBank | BF891566 |
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|    | 316441-43-7, | GenBank | BF891571 | 316441-44-8, | GenBank | BF891572 |
|    | 316441-45-9, | GenBank | BF891573 | 316441-46-0, | GenBank | BF891574 |
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|    | 316441-57-3, | GenBank | BF891585 | 316441-58-4, | GenBank | BF891586 |
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|    | 316441-73-3, | GenBank | BF891601 | 316441-74-4, | GenBank | BF891602 |
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| 316442-45-2, | GenBank      | BF891674 | 316442-46-3, | GenBank      | BF891675 |
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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(nucleotide sequence; contribution of 700,000 ORF sequence tags to the definition of the human transcriptome)

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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL  
(Biological study)

(nucleotide sequence; contribution of 700,000 ORF sequence tags to the  
definition of the human transcriptome)